

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OK protein - nucleic search, using frame_plus.p2n model

Run on: December 9, 2002, 11:31:04 ; Search time 77 Seconds
(without alignments)
3004.079 Million cell updates/sec

Title: US-09-765-034-2
1747
Perfect score: 1 MLG1MANNACTKNWLAEEA.....KSLTFSRWHELLLSFREK 334
Sequence:

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 361435 seqs, 346278564 residues

Total number of hits satisfying chosen parameters: 722870

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ .p2n.model -DEV=xlh
-O=/cgn2.1/USPTO.spool/US09765034/runat_05122002.132014.21371/app.query.fasta_1.519
-DB=Pending Patents_NA_New -OPM=fastap -SUFPIX=p2n.rnpn -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Diosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINTEN=0
-MAXLEN=200000000 -USER=US09765034.@cgn.1.1.38.@runat_05122002.132014.21371
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV.TIMEOUT=130 -WARN_TIMEOUT=30 -THREAT=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6
-FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1737	99.4	1005	6	US-10-272-983-35
2	1737	99.4	1436	6	US-10-264-237-1352
3	1720	98.5	1428	6	US-10-270-857-1
4	1720	98.5	1428	6	US-10-270-587-1
5	477	27.3	1014	6	US-10-270-144-1
6	477	27.3	1014	6	US-10-270-144-10
7	477	27.3	9905	6	US-10-270-144-3
8	384	22.0	2807	5	US-09-979-603A-1
9	384	22.0	2807	5	US-09-979-603-1
10	363.5	20.7	1922	6	US-10-152-319A-2068
11	348.5	19.9	1101	5	US-09-979-603A-17

12	348.5	19.9	1101	5	US-09-979-603-17	Sequence 17, Appl
13	343	19.6	1249	5	US-09-979-603A-21	Sequence 21, Appl
14	343	19.6	1249	5	US-09-979-603-21	Sequence 21, Appl
15	329	18.8	1451	5	US-09-958-805A-1	Sequence 1, Appl
16	323	18.5	3056	6	US-10-180-949-3	Sequence 3, Appl
17	321.5	18.4	2260	5	US-09-724-676-33307	Sequence 33307, A
18	321.5	18.4	2260	5	US-09-724-676A-33307	Sequence 33307, A
19	321.5	18.4	2279	5	US-09-724-676-33306	Sequence 33306, A
20	321.5	18.4	2279	5	US-09-724-676A-33306	Sequence 33306, A
21	321.5	18.4	2344	5	US-09-724-676-33308	Sequence 33308, A
22	321.5	18.4	2344	5	US-09-724-676A-33308	Sequence 33308, A
23	317.5	18.2	2051	6	US-10-240-425-1201	Sequence 1201, Ap
24	316	18.1	1450	6	US-10-152-319A-1852	Sequence 1852, Ap
25	313	17.9	1014	6	US-10-152-319A-1561	Sequence 1561, Ap
26	311.5	17.8	1384	6	US-10-273-575-3	Sequence 3, Appl
27	311	17.8	1285	6	PCR-US02-32094-2	Sequence 2, Appl
28	311	17.8	1285	6	US-10-265-872-2	Sequence 1866, Ap
29	311	17.8	2156	6	US-10-152-319A-1856	Sequence 2045, Ap
30	310.5	17.8	1428	6	US-10-152-319A-2045	Sequence 1, Appl
31	310.5	17.8	1904	6	US-10-180-949-1	Sequence 12, Appl
32	306	17.5	1080	6	US-10-054-616A-12	Sequence 1, Appl
33	303	17.3	1134	6	US-10-180-933-1	Sequence 1, Appl
34	301.5	17.3	1689	6	US-10-283-028-1	Sequence 1, Appl
35	299.5	17.1	1193	6	US-10-283-028-3	Sequence 3, Appl
36	299	17.1	1788	6	US-10-270-333-134	Sequence 194, App
37	296.5	17.0	1116	6	US-10-283-028-5	Sequence 5, Appl
38	295.5	16.9	1053	6	US-10-282-837-9	Sequence 9, Appl
39	295.5	16.9	1113	1	PCR-US02-35538-9	Sequence 9, Appl
40	295.5	16.9	1113	6	US-10-282-837-7	Sequence 7, Appl
41	295.5	16.9	1147	5	US-09-721-495B-1	Sequence 1, Appl
42	292.5	16.7	1053	6	US-10-272-983-21	Sequence 21, Appl
43	292	16.7	1181	1	PCR-US02-35538-13	Sequence 13, Appl
44	289.5	16.6	990	6	US-10-270-333-116	Sequence 116, App
45	288.5	16.5	1147	5	US-09-721-495B-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-10-272-983-35
Sequence 35, Application US/10272983
GENERAL INFORMATION:
APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: AREN0050
CURRENT APPLICATION NUMBER: US/10/272,983
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US/09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 35
; LENGTH: 1005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-983-35

Alignment Scores:

Pred. No.:	6.6e-159	Length:	1005
Score:	1737.00	Matches:	333
Percent Similarity:	99.70%	Conservative:	0
Best Local Similarity:	99.70%	Mismatches:	1
Query Match:	99.43%	Indels:	0
	6	Gaps:	0

US-09-765-034-2 (1-334) x US-10-272-983-35 (1-1005)

```
QY 1 MetLeuGlyIleMeValaTrpAsnAlaThrCysLysAsnTrpLeuAlaGluAla 20
    |||||
Db 1 ATGCTGGGAGCATGCGATGCGATGCAACTGGCTGGCAGCAGAGCTGCC 60

QY 21 LeuGluYsYrYrLeuSerIlePheTyrglyIleGluPheValGlyValLeuGly 40
    |||||
Db 61 CTGGAAGAGTACTACCTTCCATTTTATGGATTGAGTTCGTGGAGTCTTGGA 120

QY 41 AsnThrIleValIleValTyrglyTyrllePheSerLeuLysAsnTrpAsnSer 60
    |||||
Db 121 AATACCATGTTGTTTACGGCTACATCTCTCTGGAAGAACTGGAGACAGATATAT 180

QY 61 TyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeu 80
    |||||
Db 181 TATCTCTTAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

QY 81 ArgSerTyraAlaAsnGlyAsnTrpIleTyrglyAspValLeuCysIleSerAsnArg 100
    |||||
Db 241 AGGAGTATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 300

QY 101 ValLeuHsAlaAsnLeuTyrllePheSerIlePheLeuPheLeuPheLeuPhe 120
    |||||
Db 301 GTGCTTATGCAACCTCTATACAGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360

QY 121 TyrLeuIleIleYsYrYrProPheArgLuhIleLeuGlnYsGluPheAlaIle 140
    |||||
Db 361 TACTGTGAATTAAGTATCCTTTCCGAGACACCTCTCTGCAAAAGAAAGATTCCTAT 420

QY 141 LeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLeuProIleLeuProLeu 160
    |||||
Db 421 TTAATCTCTGGCCATTTGGGTTTACTTAACCTTAGAGTACTACCATCTCTCCCTT 480

QY 161 IleAsnProValIleThrAspAsnGlyThrCysAsnAspPheAlaSerSerGlyAsp 180
    |||||
Db 481 ATAAATCTCTTATACAGCATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 540

QY 181 ProAsnTyraAsnLeuIleTyrllePheSerMetCysLeuThrLeuLeuGlyPheLeu 200
    |||||
Db 541 CCCAATCTCAACCATTTACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600

QY 201 PheValMetCysPhePheTyrlleTyrlleAlaLeuPheLeuYsGlnArgAsnArg 220
    |||||
Db 601 TTTGTGAGTCTCTCTTATTAACAGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660

QY 221 ValAlaThrAlaLeuProLeuGluYsProLeuAsnLeuValIleMetAlaValAlaIle 240
    |||||
Db 661 GTTCTACTGCTCTGCCCCCTTGAAGAGCTCTCAACTGGCTGCTGCTGCTGCTGCTGCT 720

QY 241 PheSerValProPheTrpProTyrlleValMetArgAsnValArgIleAlaSerArgLeu 260
    |||||
Db 721 TTTCTCTGCTGCTTTTACACCTTATCAGTCTATGCGGAATGAGAGATGCTTACGCTG 780

QY 261 GlySerTrpYsGlnTyrglyCysThrGlnValValIleAsnSerPheTyrlleValThr 280
    |||||
Db 781 GGGAGTTGAGAGCATATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840

QY 281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrlleLeuGlyAsp 300
```

```
Db 841 CGGCTTTGGCTTCTGACAGTGTCAACACCTGCTCTTATTTCTTTGGAGAT 900
QY 301 HisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheYsSerLeuThrSerPhe 320
    |||||
Db 901 CACTTCAGAGCAATGCTATGATGATCACTGAGACCAACTCAATCCCTTACATCCTTT 960

QY 321 SerArgTrpAlaHisGluLeuLeuLeuSerPheArgGluYs 344
    |||||
Db 961 AGCAGATGGCTCATGAACTCTCACTTCACTTCACTGAGAAAG 1002
```

RESULT 2

US-10-264-237-1352

Sequence 1352, Application US/10264237

GENERAL INFORMATION:

APPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PA131P1

CURRENT APPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/16450

PRIOR FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: US 60/205,515

PRIOR FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 2876

SOFTWARE: PatentIn Ver. 3.1

SEQ ID NO 1352

LENGTH: 1436

TYPE: DNA

ORGANISM: Homo sapiens

US-10-264-237-1352

Alignment Scores:

Pred. No.:	1.02e-158	Length:	1436
Score:	1737.00	Matches:	333
Percent Similarity:	99.70%	Conservative:	0
Best Local Similarity:	99.70%	Mismatches:	1
Query Match:	99.43%	Indels:	0
	6	Gaps:	0

US-09-765-034-2 (1-334) x US-10-264-237-1352 (1-1436)

```
QY 1 MetLeuGlyIleMeValaTrpAsnAlaThrCysLysAsnTrpLeuAlaGluAla 20
    |||||
Db 93 ATGCTGGGAGCATGCGATGCGATGCAACTGGCTGGCAGCAGAGCTGCC 152

QY 21 LeuGluYsYrYrLeuSerIlePheTyrglyIleGluPheValGlyValLeuGly 40
    |||||
Db 153 CTGGAAGAGTACTACCTTCCATTTTATGAGATTGAGTTCGTTGGAGTCTTGGA 212

QY 41 AsnThrIleValIleValTyrglyTyrllePheSerLeuLysAsnTrpAsnSerSer 60
    |||||
Db 213 AATACCATGTTGTTTACGGCTACATCTCTCTGGAAGAACTGGAGACAGATATAT 272

QY 61 TyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeu 80
    |||||
Db 273 TATCTCTTAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 332

QY 81 ArgSerTyraAlaAsnGlyAsnTrpIleTyrglyAspValLeuCysIleSerAsnArg 100
    |||||
Db 333 AGGAGTATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 392

QY 101 ValLeuHsAlaAsnLeuTyrllePheSerIleLeuPheLeuThrPheIleAspArg 120
    |||||
Db 393 GTGCTTATGCAACCTCTATACAGATTCCTTCTCACTTTATACAGATGATGGA 452

QY 121 TyrLeuIleIleYsYrYrProPheArgGluHsIleLeuGlnYsGluPheAlaIle 140
    |||||
Db 453 TACTGTGAATTAAGTATCCTTTCCGAGAACCTCTGCAAAAGAAAGATTTGCTATT 512

QY 141 LeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLeuProIleLeuProLeu 160
    |||||
Db 513 TTAATCTCTTGGCCATTTTGGGTTTATGATTAACCTTACAGATTACTACCATCTTCCCTT 572
```

QY	161	ILLeaSPROVAlIleTHrraSPaNGlyTHrThCYaSPaSPhePalaSerSerClYasp	180
Db	573	ATTAATCTGTTATTAAGTGCATGCATGGCACCACCTGTAATGATTTTTCAGATCTTGGAAAC	632
QY	181	PRoBaNryrAsnLeuIleTySerMeCylSerThrLeuLeuGlyPheLeuIleProLeu	200
Db	633	CCCAACTGACAACCTCATTTACAGATGTGCTCAACACTGTGGGGTCTCTATTCCTCTT	692
QY	201	PheValMetCysPhePheTyrrTyrlsIleAlaLeuPheLeuLysGlnArGAsnArGln	220
Db	693	TTTGATGATGTTCTTTATTTATTCAGAAATGGCTCTTCTTCAACAGACAGGAATAGCGAG	752
QY	221	ValAlaThrAlaLeuProLeuGlnLysProLeuAsnLeuValIleMetAlaValAlaIle	240
Db	753	GTTCGCTACTGCTCTGCCCCCTTGAAAAACCTCTCAACTTGTGTATCATGGCACTGATATC	812
QY	241	PheSerValProPheThrProTyrrHisValMetArGAsnValArGIlleAlaSerArGLeu	260
Db	813	TTTCTGTGCTTTTATACACCTTATCACGTCATCGGAAATGTGGAGATCGCTTCACGCGCTG	872
QY	261	GlySerTrpLysGlnTyrrGlnCysThrGlnValValIleAsnSerPheTyrrIleValThr	280
Db	873	GGGAGTTGGAGGCGATTCAGTGCATGCACACAGCTGTCATCAATCCTTTATTCATTTGACA	932
QY	281	ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrrPheLeuLeuGlyasp	300
Db	933	CGGCGCTTTGGCTTCTTGAAACAGTGCATCAACCCCTGTCTCTATTTCTTTTGGAGAT	992
QY	301	HisPheArGAspMetLeuMetAsnGlnLeuArGHisAsnPheLysSerLeuThrSerPhe	320
Db	993	CACCTTCAGGGAGCATGTCGATGAATCAACAGTGAACACAACTTAATCCCTTACATCTTT	1052
QY	321	SerArGTrpAlaHisGlnLeuLeuLeuSerPheArGLeuLys	334
Db	1053	AGCAGATGGGCTCATGAACTCACTTCACTTTCAGAGAAAG	1094
RESULT 3			
US-10-270-857-1			
; Sequence 1, Application US/10270857			
; GENERAL INFORMATION:			
; APPLICANT: L1, Y1			
; TITLE OF INVENTION: Human G-Protein Coupled Receptor			
; FILE REFERENCE: P217C2			
; CURRENT APPLICATION NUMBER: US/10/270,857			
; PRIOR FILING DATE: 2002-10-16			
; PRIOR APPLICATION NUMBER: US 09/908,593			
; PRIOR FILING DATE: 2001-07-20			
; PRIOR APPLICATION NUMBER: US 08/781,456			
; PRIOR FILING DATE: 1997-01-10			
; PRIOR APPLICATION NUMBER: US 60/009,902			
; PRIOR FILING DATE: 1996-01-11			
; NUMBER OF SEQ ID NOS: 9			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 1			
; LENGTH: 1428			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-270-857-1			
Alignment Scores:			
Pred. No.: 4,42e-157			
Score: 1720.00			
Length: 1428			
Matches: 329			
Percent Similarity: 99.40%			
Conservative: 3			
Best Local Similarity: 98.50%			
Mismatches: 2			
Query Match: 98.45%			
Indels: 0			
DB: 6			
Gaps: 0			
US-09-765-034-2 (1-334) x US-10-270-857-1 (1-1428)			
QY	1	MetLeuGlyIleMetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaIa	20
Db	92	ATGTGGGGAGCAATGGATGAATGCAACTGTGCAGAAACTGCTGGCAGCAGAGCTGCC	151

QY 21 LeGluLysTyrTyrLeuSerLlePheThyGlyLleIleLuePheValValGlyValLeuGly 40
 Db 152 CTGGAAAGTACTACCTTTCATTTTTATGGGATAGTTCGTGGGAGTCCTTGCA 211
 QY 41 AsnThrIleValValTyrGlyTyrLlePheSerLeuLysAsnTrpAsnSerSerAsnIle 60
 Db 212 AATACCATTTGTTTACGGCTACATCTCTCTCTGAAAGAACTGGAAACACATATATT 271
 QY 61 TyrIleuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle 80
 Db 272 TATCTCTTAACTCTCTCTGCTGACTTACCTTTCTGTCACACCTCCCATGCTGATA 331
 QY 81 ArgSerTyrAlaAsnGlyAsnTrpLleTyrGlyAspValLeuCysIleSerAsnArgTyr 100
 Db 332 AGGACTTATGCCAATGCAAACTGGATATATGGAAACGTCGTCGCAATACCAACCGATAT 391
 QY 101 ValLeuHisAlaAsnLeuTyrThrSerLleLeuPheLeuThrPheIleSerIleAspArg 120
 Db 392 GGTGCTTCANGGCAACCTGTATACAGAGATCTCTTCTTCACATTTCATCACAATAGATCGA 451
 QY 121 TyrIleuLleIleLysTyrProPheArgGluHisLeuLeuGlnLysGlyLuePheAlaIle 140
 Db 452 TACTGTAAATTAAGTATACCTTCCTCCGAGAACCTTCGCAAAAAGAAAGAGTGTATAT 511
 QY 141 LeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLeuLeuProIleLeuProLeu 160
 Db 512 TTAATCTCTGGCCATCTGGGTTTATGATACTTAAAGTAACTACCACTTCCCTCCCTT 571
 QY 161 IleAsnProValIleThrAspAsnGlyTyrThrCysAsnAspPheAlaSerSerGlyAsp 180
 Db 572 AATAATCTGTATATACGCAAAATGGGACCAACCGTATATATTGTGAAATTCGAGAAC 631
 QY 181 ProAsnTyrAsnLeuLleTyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeu 200
 Db 632 CCCAACTCAACACCTCATTTACAGCATGTGTCTTAACTGTGGGGTCTCTTATCCCTCTT 691
 QY 201 PheValMetCysPhePheTyrTyrLysLleAlaLeuPheLeuLysGlnArgAsnArgGln 220
 Db 692 TTTGTGATGTGTTCTTTATATACAAAGATGTCTCTCTTCCAAAGCAGAGAAATAGGCAG 751
 QY 221 ValAlaThrAlaLeuProLeuGluLysProLeuAsnLeuValIleMetAlaValAlaIle 240
 Db 752 GTTGCTACTGCTGTGCCCCCTGAAAGAGCTCTCAACTGGTCATCATAGGCAAGTGTATC 811
 QY 241 PheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeu 260
 Db 812 TTCTGTGGCTTTTATACACCTATACAGCTCATGTGGGAATGGAGATGCGTTACGCTG 871
 QY 261 GlySerTrpLysGlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIleValThr 280
 Db 872 GCGAGTTGGAAAGCACTATCAAGTGAAGCTCAGCTGCATCAACTCTTTTACATTTGTACA 931
 QY 281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAsp 300
 Db 932 CGGCGCTGTGGCTTCTGTAAACAGTGTATCAACCTGTCTTATTTCTTTGGGGAGAT 991
 QY 301 HisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLysSerLeuThrSerPhe 320
 Db 992 CACTTCAGGAGCAATGCTGATGAATCACTGTGAGACAACTCAATCCCTTACATCCTTT 1051
 QY 321 SerArgTrpAlaHisGluLeuLeuLeuSerPheArgGlyLys 334
 Db 1052 AGCAAGATGGCTCATGAAGCTCTTACTTTCATTCAGAGAAAG 1093

RESULT 4
 US-10-270-587-1
 ; Sequence 1, Application US/10270587
 ; GENERAL INFORMATION:
 ; APPLICANT: LI, YI
 ; TITLE OF INVENTION: Human G-Protein Coupled Receptor
 ; FILE REFERENCE: PF217C2
 ; CURRENT APPLICATION NUMBER: US/10/270,587

Db 352 TATAGAGATCCTCTTCTCACCCTGTTACAGATCTTCGCTACTGTGTGATCATTCAC 411
Qy 127 ProPheargGluHisLeuLeuGlnLysGluPheAlaIleLeuIleSerLeuAlaIle 146
Db 412 CCAATGAGCTGCTTTTCATTCACAAACCTGCATGCATGTGACCTGTGCTGGTG 471
Qy 147 TrpValLeuValThrLeuGlnLeuLeuProIleLeuProLeuIleAsnProValIleThr 166
Db 472 TGGATCATTTTCAGCTAGCTACCTTCATCCGATGCATCCTTCTTATCACAACCAACAG 531
Qy 167 AspAsnGlyThrThrcysAsnAspPheAlaSerSerGlyAspProAsnTyraSerLeuIle 186
Db 532 ACCACAGATCAGCTGCTGTCTGCACCTCACCACAGTTCCGATGAGTCAATTAATAAGTG 551
Qy 187 TyrSerMetCysLeuThrLeuLeuGlnPheLeuIleProLeuPheValMetCysPhePhe 206
Db 592 TACACCTGATTTTGCATGCACACTACTTCTTCTGCTCCCTGGTGATAGAGACACTTTCG 651
Qy 207 TyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAlaLeuPro 226
Db 652 TATACACAGATTT---ATCCACACTCTGACCCAGCTGACCTCAAACTGACAGCTCCCTAAG 708
Qy 227 LeuGlnLysProLeuAsnLeuValIleMetAlaValIlePheSerValProPheThr 246
Db 709 ---CAGAAAGCAGAGAGCTAACCATTTCTGCTACTCTTGCATTTTACGTATGTTTITA 765
Qy 247 ProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrrpLysGlnTyr 266
Db 766 CCTTCATATCTTGAGGCTGATCGATCGAATCTCGCTGCTTCA-----ATC 816
Qy 267 GlnCysThr---GlnValValIleAsnSerPheTyrIleValIleThrArgProLeuAlaPhe 285
Db 817 AGTTGTCATTCAGAGATCAGATCAGATGAGCTTACATGCTTCTGACCATTAAGCTGCTG 876
Qy 286 LeuAsnSerValIleLeuAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAspMet 305
Db 877 CAGAACCTTTGCTGATCCTGTTACTATATGCTGTGCTGACGACCACTTTCAGCAGCT 936
Qy 306 LeuMetAsnGlnLeuArg 311
Db 937 GTCCTCTCAACAGTGAGA 954

RESULT 6
US-10-278-141-10
; Sequence 10, Application US/10278141
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, Chandra
; APPLICANT: LU, Dyung Alina M.
; APPLICANT: THORNTON, Michael
; APPLICANT: LU, Yan
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: GRAUL, Richard
; APPLICANT: KHAN, Fairah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: NGUYEN, Dannel B.
; APPLICANT: YUE, Henry
; APPLICANT: HAFALIA, April
; APPLICANT: ELIJOT, Vicki S.
; APPLICANT: LAL, Preeti
; APPLICANT: REDDY, Roopa
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: TANG, Y. Tom
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0096 USA
; CURRENT APPLICATION NUMBER: US/10/278,141
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 60/208,834
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/207,566
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US01/16285

; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/205,628
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 60/208,861
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/206,222
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 6575963CH1
US-10-278-141-10

Alignment Scores:
Pred. No.: 1,82e-37 Length: 1014
Score: 477.00 Matches: 110
Percent Similarity: 55.88 Conservative: 61
Best Local Similarity: 35.95 Mismatches: 123
Query Match: 27.308 Indels: 12
Gaps: 6

US-09-765-034-2 (1-334) x US-10-278-141-10 (1-1014).

Qy 8 AsnAlaThrCysLysAsnTrpLeuAlaIleAlaLeuLysTyrTyrLeuSer 27
Db 67 AATGGCACTGATGAAC-----ATCCCACTCAAGATGACATGCTCCCT 111
Qy 28 IlePheTyrGlyIleGluPheValGlyValLeuGlyAsnThrIleValValTyrGly 47
Db 112 GTTATTATTAGCATATTCCTCCGCGGGATTTCCAGGCAATGACATGATGATACCT 171
Qy 48 TyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsnLeuSerVal 67
Db 172 TACATTTTCAAAATGAGACCTTGGAAGACGACCATCATATATGCTGAACCTGGCTCG 231
Qy 68 SerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAlaSerGly 86
Db 232 ACAGATCTGCTGATCTGACCAAGCTCCCTTCTGATTCATCTACTATGCACTGGCGAA 291
Qy 87 AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHisAlaAsnLeu 106
Db 292 AACTGATCTTTGGAGATTCATGCTGATTAATCCGCTTCAGCTTCATTCACCTG 351
Qy 107 TyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIleIleLysTyr 126
Db 352 TATAGCAGATCCTCTCCCTCACCTGTTCCAGCATCTCCGCTACGCTGATCATTCAC 411
Qy 127 ProPheargGluHisLeuLeuGlnLysGluPheAlaIleLeuIleSerLeuAlaIle 146
Db 412 CCAATGAGCTGCTTTTCATTCACAAACTCGATGTCAGTGTACCTGTGCTGGTG 471
Qy 147 TrpValLeuValThrLeuGlnLeuLeuProIleLeuProLeuIleAsnProValIleThr 166
Db 472 TGGATCATTTTCAGCTAGCTACCTTCATCCGATGCATCCTTCTTATCACAACCAACAG 531
Qy 167 AspAsnGlyThrThrcysAsnAspPheAlaSerSerGlyAspProAsnTyraSerLeuIle 186
Db 532 ACCACAGATCAGCTGCTGTCTGCACCTCACCACAGTTCCGATGAGTCAATTAATAAGTG 591
Qy 187 TyrSerMetCysLeuThrLeuLeuGlnPheLeuIleProLeuPheValMetCysPhePhe 206
Db 592 TACACCTGATTTTGCATGCACACTACTTCTGCTCCCTGGTGATAGAGACACTTTCG 651
Qy 207 TyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAlaLeuPro 226
Db 652 TATACACAGATTT---ATCCACACTCTGACCCAGCTGACCTCAAACTGACAGCTCCCTAAG 708
Qy 227 LeuGlnLysProLeuAsnLeuValIleMetAlaValIlePheSerValProPheThr 246

DB: 5 Gaps: 11

US-09-765-034-2 (1-334) x US-09-979-603A-1 (1-2807)

OY 8 AsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaLeuGluLysTyr----- 24

DB 321 AATGGCACCCTTACAGCAATTAACACAGGAACTGCACCAATTGAAACTTCAAGACAGAA 380

OY 25 TyrLeuSerIlePheThrGlyIleGluPheValValGlyValLeuGlyAsnThrIleVal 44

DB 381 TTTTCCCAATGTATATCTGATATATATTTCTGGGAGCTCTGGGAAATGGTTGTC 440

OY 45 ValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsn 64

DB 441 ATATATGTTTCTCGACGCTTATTAAGAGTCCACATCTGTACAGTCTTATTCATGCTAAAT 500

OY 65 LeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAla 84

DB 501 CTGGCCATTTCAGATCTCTCTGTTCAATACACAGCTTCCCTTACGGCTGACATTAATCTT 560

OY 85 AsnGly---AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHis 103

DB 561 AGAGGCTCCAAATGGATATTTGGAGACCTGGCTGAGAGATTAATGCTTATTCCTGTAT 620

OY 104 AlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrIleUle 123

DB 621 GTCAACATGTACAGCAATTAATTTATTTCTGACCGTGTGAGTGTGGCTTCTCGGCA 680

OY 124 IleLysTyrProPheArg---GluHisLeuLeuGluLysGluPheAlaIleLeuIle 142

DB 681 ATGGTTACCCCTTTCGGCTTCTGCAATGTCACACAGCATCAGAGAGCCCTGATCCTGT 740

OY 143 SerLeuAlaIleTrpValLeuValThrLeuGluLeuProIleLeuProLeuIleAsn 162

DB 741 GGGATC---ATATGATCTCTTATCATGGCTTCTCAATATAGCTCTG----- 785

OY 163 ProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsn 182

DB 786 -----GACAGTGGCTCTGTGAGCAAGCGCATGTGTACATCA----- 821

OY 183 TyrAsnLeuIleTyrSerMetCysLeuThrLeu----- 193

DB 822 -----TGCCTTAGAGCTGAATCTGTATATAAATTCCTTAAGCTGCAG 860

OY 194 -----LeuGlyPheLeuIleProLeuPheValMetCysPhe 205

DB 861 ACCATGACTATATATGCTTGGTGGGCTGCTGCTGCTGCTGCTTTCACACTCAGACATC 920

OY 206 PheTyrTyrLys---IleAlaLeuPheLeuLysGluAsnArgGluValAlaThrAla 224

DB 921 TGTATCTGCTGATCATTCGGGTCTGTGTTAAAGTGAGAGTCCAGCAAGCGGCTGCGG 980

OY 225 LeuProLeuGluLysProLeuAsnLeuValIleMetAlaValAlaIlePheSerValPro 244

DB 981 GTTTCACAGAGAAAGCACTGCACACATCATCATCACTTGTATCTTCTTCTGTGT 1040

OY 245 PheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeuLysSerTyrLys 264

DB 1041 TTCCTGCTTATCACACACTGAGGACGCTC-----CACTTGACGACATGAGAA 1088

OY 265 GlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIleValThrArgProLeuAla 284

DB 1089 GTGGGTTTATGCAAAAGAC---AGACTGCAATAAGCTTGTGTTATCATCAGCTGGCTGGCA 1145

OY 285 PheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAsp 304

DB 1146 GCAGCCAAATGCTGCTTCAATCTCTGCTCTATTAATCTTGTGGGAGAAATTTTAAGGAC 1205

OY 305 MetLeuMetAsnGlnLeuArg-----HisAsnPheLysSerLeuThr 318

DB 1206 AGACTTAAGTCTGCACTGAGAAAGGCAATCCACAGAAAGCA 1253

US-09-979-603-1

/ Sequence 1, Application US/09979603

/ GENERAL INFORMATION:

/ APPLICANT: Yamanouchi Pharmaceutical Co. Ltd.

/ APPLICANT: Helix Research Institute

/ TITLE OF INVENTION: PEPTIDE LEUKOTRIENE RECEPTOR

/ FILE REFERENCE: 067335

/ CURRENT APPLICATION NUMBER: US/09/979,603

/ CURRENT FILING DATE: 2001-11-26

/ PRIOR APPLICATION NUMBER: PCT/JP00/06265

/ PRIOR FILING DATE: 2000-09-13

/ PRIOR APPLICATION NUMBER: JP 11-259986

/ PRIOR FILING DATE: 1999-09-14

/ NUMBER OF SEQ ID NOS: 24

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 1

/ LENGTH: 2807

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ FEATURE:

/ NAME/KEY: exon

/ LOCATION: (264)..(1301)

/ OTHER INFORMATION:

US-09-979-603-1

Alignment Scores:

Pred. No.: 5,82e-28 Length: 2807

Score: 384.00 Matches: 102

Percent Similarity: 47.92% Conservative: 59

Best Local Similarity: 30.36% Mismatches: 125

Query Match: 21.98% Indels: 50

DB: 5 Gaps: 11

US-09-765-034-2 (1-334) x US-09-979-603-1 (1-2807)

OY 8 AsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaLeuGluLysTyr----- 24

DB 321 AATGGCACCCTTACAGCAATTAACACAGGAACTGCACCAATTGAAACTTCAAGACAGAA 380

OY 25 TyrLeuSerIlePheThrGlyIleGluPheValValGlyValLeuGlyAsnThrIleVal 44

DB 381 TTTTCCCAATGTATATCTGATATATATTTCTGGGAGCTCTGGGAAATGGTTGTC 440

OY 45 ValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsn 64

DB 441 ATATATGTTTCTCGACGCTTATTAAGAGTCCACATCTGTACAGTCTTATTCATGCTAAAT 500

OY 45 ValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsn 64

DB 441 ATATATGTTTCTCGACGCTTATTAAGAGTCCACATCTGTACAGTCTTATTCATGCTAAAT 500

OY 65 LeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAla 84

DB 501 CTGGCCATTTCAGATCTCTCTGTTCAATACACAGCTTCCCTTACGGCTGACATTAATCTT 560

OY 85 AsnGly---AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHis 103

DB 561 AGAGGCTCCAAATGGATATTTGGAGACCTGGCTGAGAGATTAATGCTTATTCCTGTAT 620

OY 104 AlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrIleUle 123

DB 621 GTCAACATGTACAGCAATTAATTTATTTCTGACCGTGTGAGTGTGGCTTCTCGGCA 680

OY 124 IleLysTyrProPheArg---GluHisLeuLeuGluLysGluPheAlaIleLeuIle 142

DB 681 ATGGTTACCCCTTTCGGCTTCTGCAATGTCACACAGCATCAGAGAGCCCTGATCCTGT 740

OY 143 SerLeuAlaIleTrpValLeuValThrLeuGluLeuProIleLeuProLeuIleAsn 162

DB 741 GGGATC---ATATGATCTCTTATCATGGCTTCTCAATATAGCTCTG----- 785

OY 163 ProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsn 182

DB 786 -----GACAGTGGCTCTGAGCAAGCGCATGTGTACATCA----- 821

OY 183 TyrAsnLeuIleTyrSerMetCysLeuThrLeu----- 193

